SEARCH REQUEST FORM

Requestor's	Serial		
Name: Phone	Number: e:	Art Unit:	
Search Topic: Please write a detailed statement of search topic. Describe that may have a special meaning. Give examples or relevar a copy of the sequence. You may include a copy of the be	nt citations, authors keywords, et	c., if known. For seque	. Define any terms nces, please attach
		·····	
STA	FF USE ONLY		
Date completed: 05-23-03	Search Site	Vendors	
Searcher: Reveries 24994	STIC		IG Suite
Terminal time: 20' Elapsed time:	CM-1		STN Dialog
CPU time:	Type f Search		_
Total time: 23	N.A. Sequenc		-
Number of Searches:	A.A. Sequenc	e	SDC DARC/Questel
rounder of Databases.	Pibliographic		Other Caro

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Sequence:
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11086.992 Million cell updates/sec
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the number of results predicted by chance to have a

CDS

/organism="Homo sapiens"
/db_xref="LocusID:4796"
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/tlssue_type="Brain, neuroblastoma"
/clone_iib="NIH_MGC.19"
/lab_host="DH108-R"
/note="Vector: pOTB7"
/474. .4133

FEATURES

Location/Qualifiers 1, .4501

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 12 Row: c Column: 8 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7305310.

source

Pred. No.

is

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

AC087337 Homo sap	AC087337	Ŋ	69215	5.5	138	u	a
U16258 Human I ka	HSU16258	9	1813	13.5	340	4	
AC022505 Homo sap	AC022505	2	191078	15.8	400	w	
AJ249601 Homo sap	HSA249601	9	7543	32.5	820	2	
BC008782 Homo sapi	BC008782	9	4501	61.3	1549	1	
Description	Match Length DB ID	DB	Match Length DB	Match	Score		
				Query		Result	Re
				•			

ALIGNMENTS

	REMARK	ORGANISM REFERENCE AUTHORS TITLE JOURNAL	RESULT 1 BC008782 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE
Sequencing Center (NISC), Gaithersburg, Maryland; Gaithersburg, Maryland; Meb site: http://www.nisc.nih.gov/ Contact: nisc.mgc@chgri.nih.gov/ Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Guan,X., Gupta,J., Ho,SL., Karlins,E., Legaspi,R., Dietrich,N.L., Guan,X., Gupta,J., Ho,SL., Karlins,E., Legaspi,R., Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J., Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Zhang,LH. and Green,E.D.	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA NJH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 4501) Strausberg, R. Direct Submission Submitted (25-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer	BC008782 4501 bp mRNA linear PRI 12-JUL-2001 Homo sapiens, nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 2, clone MGC:3398 IMAGE:3628374, mRNA, complete cds. BC008782 BC008782.1 GI:14250635 MGC. Homo sapiens.

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BASE COUNT
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Best Local Similarity 99.8%;
Matches 1749; Conservative
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                                                                              ATTGCACAGGTCCTCCAAGACCTGGGAGACTTTTTGGCTGCCAAGCGAGCCCTGAAGAAG 797
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2312	3 ACTCGAAAGGGCCTCAGCCCGCTGGAGACGCTGCAGCAGTGGGTGAAGCTGTACCGCAGG	Qy :
1877	1818 TGTGGCCACTTCGAGGTGGCTGAGCTGCTTGAACGGGGGGCGTCCGTC	Db :
2252	93 TGTGGCCACTTCGAGGTGGCTGAGCTGCTGCTTGAACGGGGGGGCGTCCGTC	Qy
8		Ü
2192	133 GTGGACGACCCAGGTGGCCAGGGCTGCGAAGGCATCACCCCCCCTCCACGATGCCCTCAAC	Qy
1757	8 GAGGCCTGCAACTACGGGCATCTAGAAATTGTCCGCTTCCTGCTGGACCACGGGGCCCCA	-
2132	073 GAGGCCTGCAACTACGGGCATCTAGAAATTGTCCGCTTCCTGCTGGACCACGGGGCCGCA	Qy :
1697	638 CTTGTGAGGCAGGGCCACCCCCTTAACCCTCGGGACTACTGTGGCTGGACACCTCTGCAC	
2072	013 CTTGTGAGGCAGGGCCACCCCTTAACCCTCGGGACTACTGTGGCTGGACACCTCTGCAC	Oy :
1637	8 ATGGGGAGACCCTGCTGCACCGAGCCTGCATCGAGGCCCAGCTGCGCCCGCGTCCAGGA	
2012	953 ATGGGGGAGACCCTGCTGCACCGAGCCTGCATCGAGGGCCAGCTGCGCCGCGCGCG	
1577	518 GAGGAGCTTCAGGGCCACCTGGGCCGGCGGAAGGGGGAGCAAGTGGAACCGGCGAAACGAC	Db :
1952	893 GAGGAGCTTCAGGGCCACCTGGGCCGGCGGAAGGGGAGCAAGTGGAACCGGCGAAACGAC	
1517	4	Db :
1892	833 GTGGAGCTCTCAGAGAGGGGGAGGACGACGGGTGGCCTGACCCCGCAGCTGGAGGAGGAG	
1457	398 GAGGAGGAGGCGGAGGCGACAGCCGAGAGGCGAAGCCCTGGAGGCCGGCGAG	
1832	773 GAGGAGGAGGCGGAGGCGGCAGCCACAGCGGAGAGCGGAAGCCCTGGAGGCCGGCGAG	
1397	338 GAGGCCCCTGAGACCGAAACCAGACTGCGGGAGCTCAGTGTAGCTGAAGATGAGATGAG	Db
1772	713 GAGGCCCCTGAGACCGAAACCAGACTGCGGGAGCTCAGTGTAGCTGAAGATGAAGATGAG	
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21	158 GAGGAGGCCAAGACCTGGCTGAACATTGCACTGTCCCGCGAGGAGGCCGGCGATGCCTAC	
1592	533 GAGGAGGCCAAGACCTGGCTGAACATTGCACTGTCCCGCGAGGAGGCCGGCGATGCCTAC	Qy
15	98 CACCATGGGGCCGTGCGCCACTATGAGGAGCTGAGGCTGCGCAGCGGCAACGTGCTG	
1532	473 CACCATGGGGCCGTGCGCCACTATGAGGAGGAACTGAGGCTGCGCAGCGGCAACGTGCTG	
1097	038 GGTGCTGAGCGGGCCATCATCCACGTGTCCCTGGCCACCACGTGGGAACATGAAGGAC	Db :
1472	413 GGTGCTGAGCGGGCCATCATCCACGTGTCCCTGGCCACCACTGGGAGACATGAAGGAC	
1037	78 CCCAGGCCAGCTGAGGCTTACCAGAAGCAGCTGCGTTTTGCTGAGCTGCTGGACAGACCG	Db
1412	53 CCCAGGGCAGCTGAGGCTTACCAGAAGCAGCTGCGTTTTGCTGAGCTGCTGGACAGACC	Qy
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17	58 CATGTGCTGGCAGTGCAGCTGCAGCAGAGAGAGAGGCTGAAGAGAGACACTT	B &
1292	ATGTGCTGGCAGTGGTCCGGCTGCAGCAGCAGCTGGAAGAGCCTGAGGGCAGAGACACCT	04

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (14-SEP-1999) Norman D.A.M., Cardiothoracic Surgery, National Heart and Lung Institute, Dovehouse Street, London, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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Direct Submission
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Ann. Hum. Genet. 64 (Pt 1), 15-23 (2000)
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1 (bases 1 to 7543)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IkappaBR; NFKBIL2 gene.
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sapiens partial NFKBIL2 gene for IkappaBR, exons 1-13
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/number=J
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/db_xref="taxon:9606"
/chromosome="8"
/clone="47-g4"
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                                                                                                                                                                      join(1180. .1280,1545. .1716,1806. .1920,2847. .2992,
3088. .3240,3482. .3607,3748. .3937,5222. .5304,5399.
6862. .6934,7041. .7204,7280. .>7543)
/gene="NFKBIL2"
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3...3240,3482...3607,3748...3937,5222...5304,5399...5488,
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ASGQCKQGVPCPWGCCAYAESPRALISGDAPSQVEREVPGPCLNTHSLSHR"
1281. .1544
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Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Worley, K.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Worley, K.C.
Direct Submission
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Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bont
Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Brys
Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.
* NOTE: Estimated insert size may differ from sequence length
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                                                                                                                                                                             Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap: version 0.990329
Consensus quality: 174222 bases at least Q40
Consensus quality: 181742 bases at least Q30
Consensus quality: 186048 bases at least Q20
Estimated insert size: 185577; sum-of-contigs estimation partitions.
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Chemistry: Dye-terminator Big Dye:
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Center project name: HADS
Center clone name: RP11-349C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Baylor College of Medicine Center code: BCM
                                                                                                                                         Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
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NOTE: This is a 'working draft' sequence. It currently
consists of 21 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
the of the pieces.
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of 3121
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Homo sapiens
Eukaryota; Metazoa; Chordata;
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                      Human
U16258
                                                                                  Direct Submission
Submitted (24-OCT-1994) Anuradha Ray, Internal
Section, School of Medicine, Yale University, 3
105, New Haven, CT 06520-8057, USA
                                                                                                                                Ray,A.
                                                                                                                                                                         l (bases 325 to 1770)
Ray,P., Zhang,D.H., Elias,J.A. and Ray,A.
Cloning of a differentially expressed I kappa
J. Biol. Chem. 270 (18), 10680-10685 (1995)
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                                 /organism="Homo sapiens"
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Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagods, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T.,
                                                                                      Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastien, Y., Boguslavkiy, L., Boukhjalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 69215)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens chromosome SAMPLING.
                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                     Homo sapiens chromosome 8, clone RP11-349C2
                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                              AC087337.2 GI:20143601
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//Eransiation="MRTELYLNIGGTFESLQQTALCNDYFRKSIFLÄDENHLYEDLFR
//Eransiation="MRTELYLNIGGTFESLQQTALCNDYFRKSIFLÄDENHLYEDLFR
ARYNLGTIHWRAGQHSQAMRCLEGARECAHTMSEAVHGERVLRGYCTGPPRPRETLFGC
QASPEEALQAGLPEACAGSHLSEPPACAAVVRLQQOLEEARGRDPQGAMVICEQLGD
LPSKAGDFPRAEAYQKQLRFAELLDRPGAERAITHVSLATTLGDMKDHHGAVRHYEE
ELRLRSGNVLEEAKTWINIALSREEARCIKAAGPYLPESAQLCPGGPASPAAEAGGLAA
SPYRAARGCRFQEAFETTRLEELSVAEDEDDEEEAREAHGGETTPGRGGALREG
GRHRWPDPAAGGGRGASGPPGAAKGSKWNRRNDMGETILHRAITEGQLRRVQDLVRQG
HPLNPRDYCGWTPLHEACNYGHLEIVEFLLDHGAAVDDPGGQGCEGITPLHDALNCGH
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NAL Submitted (28-DEC-2000) Whitehead Institute/MIT Center for Genome NAL Submitted (28-DEC-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (25-200) Research, 320 Charles Street, Cambridge, MA 02141, USA (25-20) Research, 320 Charles Street, Cambridge, MA 02141, A. Allen, N. Allen, N. Anderson, S., Intoon, L., Nusbaum, C., Lander, E., Ali, A., Allen, N. Anderson, S., Compel, N., Camarata, J., Campopiano, A., Chang, J., Cohararo, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitcHugh, W., Gaye, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., MacConald, P., Major, J., Marquis, N., Matthews, C., MacCarthy, M., McGwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Petta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Stange-Thomann, N., Stojanovic, N., Stojanovic, N., Stojanovic, N., Stojanovic, N., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (12-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 12, 2002 this sequence version replaced gi:11993983. All repeats were identified using RepeatMasker: smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McRernan, K., McDeeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., McPhy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Phunkhang, P., Rise, C., Rogov, P., Roman, J., Rosetti, M., Ribeack, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Storauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Membek, I., Wu, X., Wyman, D., Ye, M.J., Young, G., Zainoun, J., Rombek, I., Timper, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone
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                                                                                                                                                                                                                                                                                                                                                                                                                     will be sequenced to completion. In the event
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L11607
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is updated, the accession number will
                            100 bp contig of 738 bp in length
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10533: contig of 700 bp
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10633: gap of
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11463: gap of
1100 bp
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14721: gap of
116258
11637: contig of 714 bp
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11637: contig of 712 bp
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11637: contig of 712 bp
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11637: contig of 712 bp
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11637: contig of 713 bp
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17170: gap of
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17170: gap of
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11939: contig of 713 bp
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17170: gap of
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8885 8984: gap of 100
8985 9724: contig of 7,
9725 9824: gap of
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                                                                38 26137: gap of 100 bp 118 26860: conti g of 723 bp in 18 26960: gap of 100 bp 161 27665: conti g of 705 bp in 18 266 2765: gap of 100 bp 166 28471: conti g of 706 bp in 18 772 28571: gap of 100 bp 172 28571: gap of 1724 bp in 18 272 28571: gap of 1724 bp in 18 28571: gap of 1
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6464: conting of
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CTGACGCAGCCTTGCCTT
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34974 35073: gap of 100 bp

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b; Pred. No. 5.2e-58;

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Search completed: May 27, 2003, 11:08:57
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ABL80248
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RESULT 1 ABL87752/c

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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 167; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing polypeptide -
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2096 AGAAATTGTCCGCTTCCTGGACCACGGGGCCCCAGTGGACCCAGGTGGCCCAGGTGGCCAGGG 2155
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                                                                                                                                                                           2156 CTGCGAAGGCATCACCCCCCTCCACGATGCCCTCAACTGTGGCCACTTCGAGGTGGCTGA 2215
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                                                                                                                                                                                                                                                                           262 AGAAATTGTCCGCTTCCTGCTGGACCACGGGGCCGCAGTGGACGACCCAGGTGGCCAGGG 203
                                                                                                                                       CTGCGAAGGCATCACCCCCCCCCCACGATGCCCTCAACTGTGGCCACTTCGAGGTGGCTGA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID 10730; 489pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 167; DB 24
Pred. No. 9e-66;
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RESULT 2
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ID ABL802.
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AC ABL802
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DT 17-MAY
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DE Human
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KW Human;
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CC (I) has cytostatic activity. An ollyonucleotide (IV) that hybridises to CC (S1) can be used for detecting ovarian cancer in a patient's biological CC sample preferably serum or ovarian tissue. The method comprises CC contacting a biological sample from a patient with (IV), detecting the amount of polynucleotide hybridising to (IV) and comparing the amount to a predetermined cutoff value and thereby detecting ovarian cancer in the patient, where the amount of polynucleotide hybridising to (IV) is detected preferably by polymerase chain reaction (PCR). (I) comprising CC (III) and/or (II) is useful for stimulating and/or expanding T cells can detected preferably by polymerase chain reaction of the tumour protein comprising CC (III) and/or (III) (III) is useful in design and preparation of CC and proteins in tumour cells; and to isolate a full length gene from a contactine in tumour cells; and to isolate a full length gene from a contactine in the contactine of the tumour polypeptides contactine in tumour cells; and to isolate a full length gene from a contactine in tumour cells; and to isolate a full length gene from a contactine in the contactine of the tumour polypeptides contactine in tumour cells; and to isolate a full length gene from a contactine of the chain cancer in the contactine of the chain cancer in the contactine of the chain cancer in the cancer in the contactine of the chain cancer in the cancer 
                                                                                                                                                                                                                               Matches 101;
                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                    2156 CTGCGAAGGCATCACCCCCCCCCCACGATGCCCTCAACTGTG 2196
                                                                                                                                    2096 AGAAATTGTCCGCTTCCTGCTGGACCACGGGGCCGCAGTGGACGACCCAGGTGGCCAGGG 2155
                                                                                                                                                                                                                                                                                                                                        Sequence 302 BP; 59 A; 96 C; 108 G; 39 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (II) of a ovarian tumour polypeptide encoded by a polynucleotide (III) having a cDNA sequence (S1) from the 10912 nucleotide sequences as given in ABL77023 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID 3226; 489pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Algate PA, Harlocker SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAY-2001; 2001WO-US17756.
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200 CTGCGAAGGCATCACCCCCCTCCACGATGCCCTCAACTGTG
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Local Similarity 100.0%; p
                                                                                                         AGAAATTGTCCGCTTCCTGCTGGACCACGGGGCCGCAGTGGACGACCCAGGTGGCCAGGG 201
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Search completed: May 27, 2003, 09:06:15
Job time : 568 secs

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Title:
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No matches found
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Gapop 60.0 , Gapext 60.0
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Dackfiles1.seq:*
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Search completed: May 27, 2003, 11:58:01 Job time : 98 secs

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                US-09-867-701-10730/c

; Sequence 10730, Application US/09867701

; Patent No. US20020132237A1

; GENERAL INFORMATION:

APPLICANT: Aglate, Paul A.

APPLICANT: Jones, Robert

APPLICANT: Harlocker, Susan L.

APPLICANT: Harlocker, Susan L.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.497
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CURRENT APPLICATION NUMBER: US/09/867,701
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US-09-867-701-3226
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NAME/KEY: misc_feature

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OTHER INFORMATION: n = A,T,C or

US-09-867-701-10730
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APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3226
LENGTH: 302
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; ORGANISM: Homo sapien
US-09-867-701-3226
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Search completed: May 27, Job time: 341 secs
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NUMBER OF SEO ID NOS: 10912
SOFTWARE: PastSEQ for Windows Version 4.0
SEO ID NO 10730
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ALIGNMENTS

AGENCOURT_7558812 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6045468 5', mRNA sequence. BQ230076 BQ230076 BG230076.1 GI:20411476 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 817) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Homo sapiens CDNA Library Preparation: Life Technologies, Inc. CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Unpublished (1999)

Query Match 27.8%; Score 703; Best Local Similarity 99.9%; Pred. No. 0;	/tissue_ /tissue_ /lab_hos /note="oo Site_2: Average full-len Note: th ASE COUNT 165 a 254	EATURES High quality sequence stop: 687. Location/Qualifiers 1. 817 source /organism="Homo sapiens /db_xref="taxon:9606" /clone="Inde::049468"
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cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution informatifound through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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Unpublished (1999)
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BM463971
                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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Mammalia; Eutheria;
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/clone_lib="NIH_MGC_72"
/clone_lib="NIH_MGC_72"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo c
Ste_2: SalI; Cloned unidirectionally. Primer: Oligo c
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CGAGGTGGCTGAGCTGCTTGAACGGGGGGGGCGTCCGTCACCCTCCGCACTCGAAAGGG 420
                                            CGAGGTGGCTGAGCTGCTTGAACGGGGGGGGCGTCCGTCACCCTCCGCACTCGAAAGGG 2263
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Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.C.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Biosch.G.E. Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
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/lab_host="DH10B (phage resistant)"
/lab_host="DH10B (phage resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."
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/db_xref="taxon:9606"
/clone="IMAGE:5492426"
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                   2029 ACCCCCTTAACCCTCGGGACTACTGTGGCTGGACACCTCTGCACGAGGCCTGCAACT.LG
                                                                                                     1969 TGCACCGAGCCTGCATCGAGGGCCAGCTGCGCCGCCTCCAGGACCTTGTGAGGCAGGGCC 2038
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                                                                   TGCACCGAGCCTGCATCGAGGGGCAGCTGCGCCGCGTCCAGGACCTTGTGAGGCAGGGCC. 125
                                                                                                                                                                                                   ACCTGGGCCGGCGGAAGGGGAGCAAGTGGAACCGGCGAAACGACATGGGGGAGACCCTGC 1968
                                                                                                                                                                                                                                              GCGAGGACGACCGATGGCCTGACCCCGCAGCTGGAGGAGGACGAGGAGCTTCAGGGCC 105
1170 bp mRNA linear EST 05-FEB-200. AGENCOURT_6485291 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5555018 5', mRNA sequence.
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Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1170)
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                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus: Vector: pcMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT
Average insert size 2.1 kb. "
a 420 c 332 g 177 t 1 others
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/db_xref="taxon:9606"
/clone="IMAGE:5555018"
/clone_lib="NIH_MGC_71"
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99.8%;
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Pred. No. 9e-225;
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High quality sequence stop: 662.
Location/Qualifiers
1. 929
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 929)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue procurement: AFCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.linl.gov
plate: LLCM18 row: g column: 12
High quality sequence stop: 661.
Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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/tissue_type="choriocarcinoma"
/lab_host="DBIOB (phage resistant)"
/lab_host="DBIOB (phage resistant)"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:3630371"
/clone_lib="NIH_MGC_21"
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/db_xref="taxon:9606"
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AGENCOURT_6739552 NIH_MGC_99 Homo sapiens cDNA clone
5', mRNA sequence.
EQ057501
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Tissue Procurement: Lou Staudt
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NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                              Plate: LLCM2064
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
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a 200 c 246 g 86 t
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                                        /organism="Homo sapiens"
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at Baylor College of Medicine
1102 Bates, MC3-3320 Houston, TX 77030,
Tel: 832-825-4038
                                                                                                                                                                                                                                                                                                                                                                                                                            BM193972

492 bp mRNA linear EST 13-DEC-20
TCAAP1E5856 Pediatric pre-B cell acute lymphoblastic leukemia
Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCAAP5856, mRNA
                                                                                      Unpublished (2001)
Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
                                                                                                                                                           1 (bases 1 to 492)
wei, Y. Tsang, Y.T. M., Mei, G., Ku, J. M., Ali-Osman, F.R. Jr.,
Gunaratne, P. H., Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.F.
Pediatric Leukemia cDNA Sequencing Project (2001)
                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                       sequence.
BM193972
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/tlssue_type="lymphoma, cell goTB); Site_1: XhoI; Site_2:
/note="Organ: lymph; Vector: goTB); Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCACGAO(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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Pred. No. 3e-103;
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Email: clones@txccc.org

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ACCESSION
VERSION
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601298526F1 NIH_MGC_19 Homo
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Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 421)
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                                                                                                                                                  BE383502
                                                                                                                                                               mRNA sequence.
                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                            Homo sapiens
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                                                                                                           human
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/lab_host="DH10B"
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/cell_type="pre-B cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Pediatric pre-B cell acute lymphoblastic
leukemia_Baylor-HGSC project=TCBA"
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/clone="TCAAP5856"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
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Pred. No. 6.6e-83;
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s cDNA clone
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AUTHORS
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BF314727
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Matches 180; Conserv
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CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
plate: LLCM1027 row: b column: 20
High quality sequence stop: 575.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Ammmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1101)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
BF314727
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/clone_lib="NIH_MGC_19"
/clone_lib="NuH_MGC_19"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
/note-motor: GCACCAGG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
/note: haboratory of Gerald M. Rubin (University of
/california, Berkeley) using ZAP-cDMA synthesis kit
/Stratagene) and Superscript II RT (Life Technologies).
/note: this is a NIH_MGC Library."
/note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
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AI733922/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            312 AGGGCCTGGGCCACCATCGGCCGCACCCACCTGGACATCTATGACCACTGCCAGTCGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372 GATGCTTTGCTGCAGGCACAGGCTGCCTTTGAGAAGAGCTTGGCTATTGTGGATGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  753 GATGCTTTGCTGCAGGCACAGGCTGCCTTTGAGAAGAGCTTGGCTATTGTGGATGAGGAG 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                zt55h12.y5 Soares ovary IMAGE:726311 5' similar
                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced human clone Original clone citation: WashU-NCI human EST Project This read has been verified (found to hit its original self in its content of the content of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
Other_ESTs: zt55h12.sl
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
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                                                                                                                                                                                                                                                                                                  Insert Length: 633    Std Erro
Seg primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                             Possible reversed clone: similarity on wrong strand Insert Length: 633 Std Error: 0.00
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2: footed; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MCC Library."

18 a 311 c 340 g 132 t
                                                                                                                                                                                                                                                           quality sequence stop: 442.
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/clone="IMAGE:4130611"
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                               /organism="Homo sapiens"
/db_xref="GDB:5938403"
/db_xref="taxon:9606"
/clone="IMAGE:726311"
                                                                                                                                                                                                                   Location/Qualifiers
/clone_lib="Soares ovary tumor NbHOT"
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; Pred. No. 4.7e-76;
0; Mismatches 0;
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tumor NbHOT Homo sapiens cDNA clone
to TR:Q13006 Q13006 I KAPPA BR.;,
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                                                                              FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
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                                                                                                                                                                                                                                                                                                                                                           TITLE
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                               JOURNAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2216 GCTGCTGCTTGAACGGGGGGCGTCCGTCACCCTCCGCACTCGAAAGG 2262
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AI820902
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                                                                                                                                                                                                                                                                              Other_ESTs: zt39d01.x5
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 503)
                                                                                                                                                                                                                     This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced human clone original clone citation: WashU-NCI human EST Project
                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI820902.1
                                                                                                                        Putative full length read
The vector to vector length is 581
Possible reversed clone: similarity
Insert Length: 639 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                             National Cancer Institute, Cancer Genome
                                                                                                                                                                                                                                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                           High quality sequence stop: 465.
Location/Qualifiers
                                                                                                                                                                                      This read has been verified (found to hit its original self in the correct orientation)
                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                             primer: -40RP from Gibco
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/db_xref="GDB:5936350"
/db_xref="taxon:9606"
/clone="mMAGE:724705"
                                                                  1. .503
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Pred. No. 8.7e-70;
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                                                                                                                                          wrong strand
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                                                                                                                                                                                                                                                                                                                                                              Anatomy Project (CGAP),
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/clone_lib="Soares ovary

tumor NbHOT"

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REFERENCE
AUTHORS
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BF111950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997) . Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 543)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Career Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BF111
                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHSF pool 1: 309384-310919, 323208-325895 Soares NbHSF pool 1: 309384-310919, 323208-325895 Soares NbHSF pool 1:
                                                                                                                                                                 /note-"Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro.
                                                                                                                                                                                                                                                                   /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:3523585"
                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
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100.0%; Pred. No. 8.8e-70;
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Best Local Similarity
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Best Local Similarity
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    148;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLANIO468 row: k column: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 699)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 578.
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  Conservative
                                                                                                   /tissue_type="embryonal carcinoma, cell line"
/lab_host="NH10B (phage-resistant)"
/note="Organ: testis; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NHH_MGC Library."
a 221 c 222 g 107 t
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                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4539789"
/clone_lib="NIH_MGC_92"
                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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RESULT 15
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                                                                     Matches 136;
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2096 AGAAATTGTCCGCTTCCTGCTGGACCACGGGGCCGCAGTGGACGACCCAGGTGGCCAGGG 2155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
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                                                                                        Local Similarity
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AI821538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced human clone Original clone citation: see original entry for original citation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            zt39d01.x5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724705 3' similar to TR:Q13006 Q13006 I KAPPA BR. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Possible reversed clone: similarity on wrong strand Insert Length: 639 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This 3' resequenced clone has no previous 3' data to
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 506)
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quality sequence stop: 463.
                                                                     Conservative 0;
                                                                                                                                                                                                   (Pharmacia). Library constructed by Bento Soares and \mathbf{M}.\mathtt{Fatima} Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="GDB:5936350"
/db_xref="taxon:9606"
/clone="IMAGE:724705"
                                                                                                                                                                                                                                                                                                                                                              /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Soares ovary tumor NbHOT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                          143 c
                                                                                                        5.48;
                                                                                   Score 136; DB 9; Pred. No. 1e-54;
                                                                                                                                                     161 g
                                                                   Mismatches
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                                                                     0;
                                                                                                 Length 506;
                                                                                                                                                        2 others
                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 24-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   verify this
                                                                 Gaps
                                                                     0
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